

SEQUENCE LISTING

<110> SOLOMON, Beka
FRENKEL, Dan

<120> IMMUNIZATION AGAINST AMYLOID PLAQUES USING DISPLAY TECHNOLOGY

<130> SOLOMON=2A

<140> US 09/473,653

<141> 1999-12-29

<150> US 60/152,417

<151> 1999-09-03

<160> 26

<170> PatentIn version 3.0

<210> 1

<211> 4

<212> PRT

<213> Artificial

<220>

<223> synthetic peptide

<400> 1

Glu Phe Arg His

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<210> 2

<211> 15

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1 5 10 15

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<211> 43

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<213> Artificial

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<400> 3

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
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Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
 20 25 30

Gly Leu Met Val Gly Gly Val Val Ile Ala Thr
 35 40

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<220>
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<400> 4

Trp Val Leu Asp
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 <211> 717
 <212> DNA
 <213> Homo sapiens

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 <221> CDS
 <222> (1)..(717)

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 Gln Val Lys Leu Gln Glu Ser Gly Ala Glu Leu Val Arg Pro Gly Val
 1 5 10 15
 tca gtg aag att tcc tgc aag ggt tct ggc tac aca ttc act gat tat 96
 Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30
 gct atg cac tgg gtg aag cag agt cat gca aag agt cta gag tgg att 144
 Ala Met His Trp Val Lys Gln Ser His Ala Lys Ser Leu Glu Trp Ile
 35 40 45
 gga gtt att agt act tac tat ggt gat gct agc tac aac cag aag ttc 192
 Gly Val Ile Ser Thr Tyr Tyr Gly Asp Ala Ser Tyr Asn Gln Lys Phe
 50 55 60
 aag ggc aag gcc aca atg act gta gac aaa tcc tcc agc aca gcc tat 240
 Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 atg gaa ctt gcc aga ctg aca tct gag gat tct gcc atc tat tac tgt 288
 Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys
 85 90 95
 gca aga ggg gct act atg tcc tac ttt gac tac tgg ggc caa gtg acc 336
 Ala Arg Gly Ala Thr Met Ser Tyr Phe Asp Tyr Trp Gly Gln Val Thr
 100 105 110

acg gtc acc gtc tcc tca ggt gga ggc ggt tca ggc gga gtt ggc tct 384
Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Val Gly Ser
115 120 125

ggc ggt ggc gga tcg gac atc gag ctc act cag tct cca gca atc atg 432
Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met
130 135 140

tct gca tct cca ggg gag aag gtc acc atg acc tgc agt gcc agc tca 480
Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser
145 150 155 160

agt ata agt tac atg cac tgg tat cag cag aag cca ggc acc tcc ccc 528
Ser Ile Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Thr Ser Pro
165 170 175

aaa aga tgg att tat gac aca tcc aaa ctg gct tct gga gtc cct gct 576
Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala
180 185 190

cgc ttc agt ggc agt ggg tct ggg acc tct tat tct ctc aca atc agc 624
Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
195 200 205

agc atg gag gct gaa gat gct gcc act tat tac tgc cat cag cgg agt 672
Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Ser
210 215 220

agt tac cca ttc acg ttc gga ggg ggg gcc aag ctg gaa ata aaa 717
Ser Tyr Pro Phe Thr Phe Gly Gly Gly Ala Lys Leu Glu Ile Lys
225 230 235

<210> 6
<211> 239
<212> PRT
<213> Homo sapiens

<400> 6

Gln Val Lys Leu Gln Glu Ser Gly Ala Glu Leu Val Arg Pro Gly Val
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Ala Met His Trp Val Lys Gln Ser His Ala Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Ser Thr Tyr Tyr Gly Asp Ala Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys
85 90 95

Ala Arg Gly Ala Thr Met Ser Tyr Phe Asp Tyr Trp Gly Gln Val Thr
100 105 110

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Val Gly Ser
115 120 125

Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met
130 135 140

Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser
145 150 155 160

Ser Ile Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Thr Ser Pro
165 170 175

Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala
180 185 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
195 200 205

Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Ser
210 215 220

Ser Tyr Pro Phe Thr Phe Gly Gly Gly Ala Lys Leu Glu Ile Lys
225 230 235

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<400> 7

Tyr Tyr Glu Phe Arg His
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<210> 8
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<223> synthetic peptide

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Val His Glu Pro His Glu Phe Arg His Val Ala Leu Asn Pro Val
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<400> 9

Lys Leu His
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<210> 10

<211> 45

<212> DNA

<213> Artificial

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<223> primer

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<221> misc_feature

<223> "n" at position 17 is unknown

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<211> 24

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 11

atctatgcgg ccagccggc catg

24

<210> 12

<211> 38

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 12
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38

<210> 13
<211> 58
<212> DNA
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<220>
<223> primer

<400> 13
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58

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<211> 52
<212> DNA
<213> Artificial

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<400> 14
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52

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His Gln Arg Ser Ser Tyr Pro Cys Thr
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His Gln Arg Ser Ser Tyr Pro Cys Thr
1 5

<210> 17
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<212> PRT
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<400> 17

His Gln Arg Ser Ser Tyr Pro Phe Thr
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<210> 18
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<400> 18

His Gln Arg Ser Ser Tyr Pro Tyr Thr
1 5

<210> 19
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<212> PRT
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His Gln Arg Ser Ser Tyr Pro Phe Thr
1 5

<210> 20
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His Gln Arg Ser Ser Tyr Pro Ser Thr
1 5

<210> 21
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Asp Thr Glu Phe Arg His Ser Ser Asn Asn Phe Ser Ala Val Arg
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<210> 22

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Ser Thr Glu Phe Arg His Gln Thr Thr Pro Leu His Pro Asn Ser
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<210> 23

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<400> 24

Ser Ala Ala Asp Phe Arg His Gly Ser Pro Pro Ile Ser Ala Phe
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<212> DNA

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<221> CDS

<222> (1)..(357)

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1 5 10 15

48

ctc act cag tct cca gca atc atg tct gca tct cca ggg gag aag gtc	96
Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val	
20 25 30	
acc atg acc tgc agt gcc agc tca agt ata agt tac atg cac tgg tat	144
Thr Met Thr Cys Ser Ala Ser Ser Ser Ile Ser Tyr Met His Trp Tyr	
35 40 45	
cag cag aag cca ggc acc tcc ccc aaa aga tgg att tat gac aca tcc	192
Gln Gln Lys Pro Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser	
50 55 60	
aaa ctg gct tct gga gtc cct gct cgc ttc agt ggc agt ggg tct ggg	240
Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly	
65 70 75 80	
acc tct tat tct ctc aca atc agc agc atg gag gct gaa gat gct gcc	288
Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala	
85 90 95	
act tat tac tgc cat cag cgg agt agt tac cca ttc acg ttc gga ggg	336
Thr Tyr Tyr Cys His Gln Arg Ser Ser Tyr Pro Phe Thr Phe Gly Gly	
100 105 110	
ggg gcc aag ctg gaa ata aaa	357
Gly Ala Lys Leu Glu Ile Lys	
115	

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<400> 26

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35 40 45	
Gln Gln Lys Pro Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser	
50 55 60	
Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly	
65 70 75 80	
Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala	
85 90 95	
Thr Tyr Tyr Cys His Gln Arg Ser Ser Tyr Pro Phe Thr Phe Gly Gly	
100 105 110	
Gly Ala Lys Leu Glu Ile Lys	
115	